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## Sim

[Click here](#) to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

[Click here](#) to download LALNVIEW (Unix, Mac and PC versions available).  
 You can also have a look at a sample screen of LALNVIEW and access its documentation.

*Results of SIM with:*

[alignment of SEQ ID NO:4 and 17](#)

Sequence 1: UserSeq4, (654 residues)  
 Sequence 2: UserSeq17, (1246 residues)

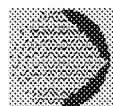
*using the parameters:*

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

100.0% identity in 654 residues overlap; Score: 3446.0; Gap frequency: 0.0%

UserSeq4, 1 QVLKGRMDSEQSPSIGYSSRTLGPNGPLILQALTLSNASDGFNLERLEMLGDSFLKHAIT  
 UserSeq17, 593 QVLKGRMDSEQSPSIGYSSRTLGPNGPLILQALTLSNASDGFNLERLEMLGDSFLKHAIT  
 \*\*\*\*\*

UserSeq4, 61 TYLFCYPDAHEGRLSYMRSKKVSNCLYRLGKKGLPSRMVVSIFDPPVNWLPPGYVVN  
 UserSeq17, 653 TYLFCYPDAHEGRLSYMRSKKVSNCLYRLGKKGLPSRMVVSIFDPPVNWLPPGYVVN  
 \*\*\*\*\*

UserSeq4, 121 QDKSNTDKWEKDEMTKDCMLANGKLDDEDYEEEDEEEESLMWRAPKEEADYEDDFLEYDQE  
 UserSeq17, 713 QDKSNTDKWEKDEMTKDCMLANGKLDDEDYEEEDEEEESLMWRAPKEEADYEDDFLEYDQE  
 \*\*\*\*\*

UserSeq4, 181 HIRFIDNMLMGSGAFVKKISLSPFSTTDSAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDA  
 UserSeq17, 773 HIRFIDNMLMGSGAFVKKISLSPFSTTDSAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDA  
 \*\*\*\*\*

UserSeq4, UserSeq17,	241	MCYLDPSKAVEEDFVVGFWNPSEENCGVDTGKQSISYDLHTEQCIADKSIADCVEALLG
	833	MCYLDPSKAVEEDFVVGFWNPSEENCGVDTGKQSISYDLHTEQCIADKSIADCVEALLG
		*****
UserSeq4, UserSeq17,	301	CYLTSCGERAAQLFLCSLGLKVLPIKRTDREKALCPTRENFSQQKNLSVSCAAASVAS
	893	CYLTSCGERAAQLFLCSLGLKVLPIKRTDREKALCPTRENFSQQKNLSVSCAAASVAS
		*****
UserSeq4, UserSeq17,	361	SRSSVLKDSEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKINYRFKNKAYLLQAFT
	953	SRSSVLKDSEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKINYRFKNKAYLLQAFT
		*****
UserSeq4, UserSeq17,	421	HASYHYNTITDCYQRLEFLGDAILDYLITKHYEDPRQHSPGVTLDRSALVNNTIFASL
	1013	HASYHYNTITDCYQRLEFLGDAILDYLITKHYEDPRQHSPGVTLDRSALVNNTIFASL
		*****
UserSeq4, UserSeq17,	481	AVKYDYHKYFKAVSPELFHVIDDFVQFQLEKNEMQGMDSELRRSEEDEEKEEDIEVPKAM
	1073	AVKYDYHKYFKAVSPELFHVIDDFVQFQLEKNEMQGMDSELRRSEEDEEKEEDIEVPKAM
		*****
UserSeq4, UserSeq17,	541	GDIFESLAGAIYMDSGMSLETWQVYYPMMRPLIEKFSANVPRSPVRELLEMEPETAKFS
	1133	GDIFESLAGAIYMDSGMSLETWQVYYPMMRPLIEKFSANVPRSPVRELLEMEPETAKFS
		*****
UserSeq4, UserSeq17,	601	PAERTYDGKVRVTVEVVGKGKFKGVGRSYRIAKSAAARRALRSLKANQPQVPNS
	1193	PAERTYDGKVRVTVEVVGKGKFKGVGRSYRIAKSAAARRALRSLKANQPQVPNS
		*****

39.0% identity in 41 residues overlap; Score: 64.0; Gap frequency: 0.0%

39.0% identity in 41 residues overlap; Score: 64.0; Gap frequency: 0.0%

UserSeq4, 45 ERLEMLGDSFLKHAITYLFCTYPDAHEGRLSYMRSKKVSN  
UserSeq17, 1026 QRLEFLGDAILDYLITKHYEDPRQHSPGVLTDLRSALVNN  
                  \*\*\* \* \*\*\* \*    \*\*    \*                    \* \*    \* \*    \* \*    \* \*

28.8% identity in 52 residues overlap; Score: 50.0; Gap frequency: 0.0%

28.8% identity in 52 residues overlap; Score: 50.0; Gap frequency: 0.0%

UserSeq4, 205 STTDSAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDAMCYLDPSKAVEEDDFV  
UserSeq17, 716 SNTDKWEKDEMTKDCMLANGKLDEDYEEEDEEEESLMWRAPKEEADYEDDFL